# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: _10/585,620_

Source: _IFWP_

Date Processed by STIC: _7/21/06_

# *ENTERED*

# CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/585,620_          CRF Edit Date: _7/21/06_
                                      Edited by: _AL_

____ Realigned nucleic acid/amino acid numbers/text  in cases where the sequence
     text "wrapped" to the next line


____ Corrected the SEQ ID NO.  Sequence numbers edited were:

     _____


____ Inserted or corrected a nucleic number at the end of a nucleic line.  SEQ ID
     NO's  edited:

     _____

__J__ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers


____ Inserted mandatory headings/numeric identifiers, specifically:

     _____


____ Moved responses to same line as heading/numeric identifier, specifically:

     _____


____ Other:

     _____
     _____
     _____

IFW*p*

RAW SEQUENCE LISTING                    DATE: 07/21/2006
PATENT APPLICATION:  US/10/585,620      TIME: 17:42:23

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\07212006\J585620.raw**

```
 3 <110> APPLICANT: Ye, Liu
 4        Lan, Tang
 5        Spendler, Tina
 7 <120> TITLE OF INVENTION: Amylase
 9 <130> FILE REFERENCE: 10583.204-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/585,620
C--> 11 <141> CURRENT FILING DATE: 2006-07-08
11 <160> NUMBER OF SEQ ID NOS: 17
13 <170> SOFTWARE: PatentIn version 3.3
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 1946
17 <212> TYPE: DNA
18 <213> ORGANISM: Chaetomium sp.
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (86)..(1843)
25 <220> FEATURE:
26 <221> NAME/KEY: sig_peptide
27 <222> LOCATION: (86)..(145)
29 <220> FEATURE:
30 <221> NAME/KEY: mat_peptide
31 <222> LOCATION: (146)..(1843)
33 <400> SEQUENCE: 1
34 tcccggtcat cctctcttgg tccctgccat cctcctgccc cctctgatcc accgcctctt        60
36 cggtggactc caagacgttg tcagg atg cga tcc ttc ctc gcc ctc tca gcc       112
37                                Met Arg Ser Phe Leu Ala Leu Ser Ala
38                                -20                 -15
40 ttg ctg ctg ctg tac ccg ctg cag ctg ctc gcc gcc agc aac tcc gac       160
41 Leu Leu Leu Leu Tyr Pro Leu Gln Leu Leu Ala Ala Ser Asn Ser Asp
42     -10                 -5              -1  1                   5
44 tgg agg tcc cgc aat atc tac ttt gcc ttg acc gac cgc gtc gcc aat       208
45 Trp Arg Ser Arg Asn Ile Tyr Phe Ala Leu Thr Asp Arg Val Ala Asn
46                 10                  15                  20
48 ccg tcc acc acg acc gca tgt agt gac ctg agc aac tac tgc ggc ggc       256
49 Pro Ser Thr Thr Thr Ala Cys Ser Asp Leu Ser Asn Tyr Cys Gly Gly
50             25                  30                  35
52 acg tgg agc ggc ctg tcg agc aag ctg gac tac atc caa ggg atg ggc       304
53 Thr Trp Ser Gly Leu Ser Ser Lys Leu Asp Tyr Ile Gln Gly Met Gly
54         40                  45                  50
56 ttc gat tcc atc tgg att acc ccc gtg gtc gag aac tgc gac ggt ggc       352
57 Phe Asp Ser Ile Trp Ile Thr Pro Val Val Glu Asn Cys Asp Gly Gly
58     55                  60                  65
60 tac cac ggc tac tgg gcc aag gcg ctc tac aac gtc aac acg aac tac       400
```

```
61 Tyr His Gly Tyr Trp Ala Lys Ala Leu Tyr Asn Val Asn Thr Asn Tyr
62 70              75              80              85
64 ggc agt gcg gat gat ctg aag aac ttc gtt gcg gcc gcc cat gcg aag    448
65 Gly Ser Ala Asp Asp Leu Lys Asn Phe Val Ala Ala Ala His Ala Lys
66              90              95              100
68 ggc atg tac gtg atg gtg gac gtc gtc gcg aat cac atg ggt tcc tgc    496
69 Gly Met Tyr Val Met Val Asp Val Val Ala Asn His Met Gly Ser Cys
70              105             110             115
72 ggc atc gcc aac ctc tcc cca cct ccc ctg aac gag cag agc tct tat    544
73 Gly Ile Ala Asn Leu Ser Pro Pro Pro Leu Asn Glu Gln Ser Ser Tyr
74              120             125             130
76 cac acc cag tgc gac att gac tac agc agt cag tcc agc att gag acg    592
77 His Thr Gln Cys Asp Ile Asp Tyr Ser Ser Gln Ser Ser Ile Glu Thr
78      135             140             145
80 tgc tgg ata tcc ggc ctc cct gac ctg gac acc acc gat agc act atc    640
81 Cys Trp Ile Ser Gly Leu Pro Asp Leu Asp Thr Thr Asp Ser Thr Ile
82 150             155             160             165
84 cga tcc ctc ttc cag acc tgg gtc cac ggc ctg gtc agc aac tac agc    688
85 Arg Ser Leu Phe Gln Thr Trp Val His Gly Leu Val Ser Asn Tyr Ser
86              170             175             180
88 ttc gac ggt ctc cgc gtc gac acc gtc aag cac gtg gag aag gat tac    736
89 Phe Asp Gly Leu Arg Val Asp Thr Val Lys His Val Glu Lys Asp Tyr
90              185             190             195
92 tgg ccc ggc ttc gtg tcg gcg gcg ggc acc tac gcc atc ggc gaa gtc    784
93 Trp Pro Gly Phe Val Ser Ala Ala Gly Thr Tyr Ala Ile Gly Glu Val
94      200             205             210
96 ttc tcc ggc gac acc tcc tac gtg gcc ggc tat caa tcg gtg atg ccg    832
97 Phe Ser Gly Asp Thr Ser Tyr Val Ala Gly Tyr Gln Ser Val Met Pro
98      215             220             225
100 ggc ttg ctc aac tat ccc atc tac tat ccg ctc atc cgc gtc ttc gcg   880
101 Gly Leu Leu Asn Tyr Pro Ile Tyr Tyr Pro Leu Ile Arg Val Phe Ala
102 230             235             240             245
104 cag ggt gcg tcc ttc acc gat ctc gtc aac aac cac gat acc gtc ggc   928
105 Gln Gly Ala Ser Phe Thr Asp Leu Val Asn Asn His Asp Thr Val Gly
106              250             255             260
108 tcg acc ttc tcc gac ccg acg ctg ctg ggt aac ttt atc gac aac cac   976
109 Ser Thr Phe Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Asp Asn His
110              265             270             275
112 gac aac cca cgt ttc ctg agc tac acc agc gac cac gcc ctc ctc aag  1024
113 Asp Asn Pro Arg Phe Leu Ser Tyr Thr Ser Asp His Ala Leu Leu Lys
114              280             285             290
116 aac gct ctg gcc tac gtc atc ctg gcc aga ggc atc ccc atc gtc tac  1072
117 Asn Ala Leu Ala Tyr Val Ile Leu Ala Arg Gly Ile Pro Ile Val Tyr
118      295             300             305
120 tac ggc acc gag caa ggc tac tcg ggt tcg tcc gac ccg gcg aac cgc  1120
121 Tyr Gly Thr Glu Gln Gly Tyr Ser Gly Ser Ser Asp Pro Ala Asn Arg
122 310             315             320             325
124 gag gat ctc tgg cgt agc gga tac agc act acg gga gac atc tac acc  1168
125 Glu Asp Leu Trp Arg Ser Gly Tyr Ser Thr Thr Gly Asp Ile Tyr Thr
```

```
126                    330                   335                    340
128 acc atc gcc gcg ctc tcc gcc gcg cgc acc gcg gcc ggt ggc ctc gcc      1216
129 Thr Ile Ala Ala Leu Ser Ala Ala Arg Thr Ala Ala Gly Gly Leu Ala
130                    345                   350                    355
132 ggt aac gac cac gtc cac ctg tac acg acc gac aac gcg tac gcc tgg      1264
133 Gly Asn Asp His Val His Leu Tyr Thr Thr Asp Asn Ala Tyr Ala Trp
134                    360                   365                    370
136 tcc cgg gcg agc ggc aag ctc atc gtc gtc acg tcc aac cgc ggc agc      1312
137 Ser Arg Ala Ser Gly Lys Leu Ile Val Val Thr Ser Asn Arg Gly Ser
138        375                   380                   385
140 tcc gac agc agc acc atc tgc ttc agc acc cag cag gcc agc ggc acc      1360
141 Ser Asp Ser Ser Thr Ile Cys Phe Ser Thr Gln Gln Ala Ser Gly Thr
142 390                   395                   400                    405
144 acc tgg acc agc acg atc acc ggc aac tcg tac acc gcc gac agc aac      1408
145 Thr Trp Thr Ser Thr Ile Thr Gly Asn Ser Tyr Thr Ala Asp Ser Asn
146                    410                   415                    420
148 ggc cag atc tgc gtg cag ctg tcc agc ggc gga ccc gag gcg ctc gtc      1456
149 Gly Gln Ile Cys Val Gln Leu Ser Ser Gly Gly Pro Glu Ala Leu Val
150                    425                   430                    435
152 gtc tcc acc gcg acc ggc acc gcc acc gcg acg act ctg tcc acg acc      1504
153 Val Ser Thr Ala Thr Gly Thr Ala Thr Ala Thr Thr Leu Ser Thr Thr
154        440                   445                   450
156 acc aag acg tcc acc tcg acc gcc tcc tgc gcc gcc acc gtc gcc gtc      1552
157 Thr Lys Thr Ser Thr Ser Thr Ala Ser Cys Ala Ala Thr Val Ala Val
158        455                   460                   465
160 acc ttc aac gag ctc gtc acc acg aac tac ggc gac acc atc cgc ctg      1600
161 Thr Phe Asn Glu Leu Val Thr Thr Asn Tyr Gly Asp Thr Ile Arg Leu
162 470                   475                   480                    485
164 acg ggc tcc atc tcc cag ctc agc agc tgg agc gca acc tcc ggg ctg      1648
165 Thr Gly Ser Ile Ser Gln Leu Ser Ser Trp Ser Ala Thr Ser Gly Leu
166                    490                   495                    500
168 gcc ctg agc gcg tcc gcg tac acg tcc agc aac ccg ctc tgg agc gtg      1696
169 Ala Leu Ser Ala Ser Ala Tyr Thr Ser Ser Asn Pro Leu Trp Ser Val
170        505                   510                   515
172 acg gtc agc ctg ccg gcc ggc acg tcg ttc gag tac aag ttc gtc cgc      1744
173 Thr Val Ser Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe Val Arg
174        520                   525                   530
176 atc acg agc gac ggc acc gtg acc tgg gaa tcg gac ccg aac cgc agc      1792
177 Ile Thr Ser Asp Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Arg Ser
178        535                   540                   545
180 tac acc gtc ccg acg tgc gcg agc acc gcg acg atc agc aat acc tgg      1840
181 Tyr Thr Val Pro Thr Cys Ala Ser Thr Ala Thr Ile Ser Asn Thr Trp
182 550                   555                   560                    565
184 cgg tgagctctgg acgtgttgta catataggag gccgttgaga ggccggggcg          1893
185 Arg
188 gttggtggtc ggggtgaatg gggggttgat gctttttcgt tgtgtcggtg aga          1946
191 <210> SEQ ID NO: 2
192 <211> LENGTH: 586
193 <212> TYPE: PRT
```

```
194 <213> ORGANISM: Chaetomium sp.
196 <400> SEQUENCE: 2
198 Met Arg Ser Phe Leu Ala Leu Ser Ala Leu Leu Leu Leu Tyr Pro Leu
199 -20                -15                 -10                     -5
202 Gln Leu Leu Ala Ala Ser Asn Ser Asp Trp Arg Ser Arg Asn Ile Tyr
203             -1  1               5                   10
206 Phe Ala Leu Thr Asp Arg Val Ala Asn Pro Ser Thr Thr Thr Ala Cys
207         15                  20                  25
210 Ser Asp Leu Ser Asn Tyr Cys Gly Gly Thr Trp Ser Gly Leu Ser Ser
211     30                  35                  40
214 Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Asp Ser Ile Trp Ile Thr
215 45                  50                  55                      60
218 Pro Val Val Glu Asn Cys Asp Gly Gly Tyr His Gly Tyr Trp Ala Lys
219                 65                  70                  75
222 Ala Leu Tyr Asn Val Asn Thr Asn Tyr Gly Ser Ala Asp Asp Leu Lys
223         80                  85                  90
226 Asn Phe Val Ala Ala Ala His Ala Lys Gly Met Tyr Val Met Val Asp
227         95                  100                 105
230 Val Val Ala Asn His Met Gly Ser Cys Gly Ile Ala Asn Leu Ser Pro
231     110                 115                 120
234 Pro Pro Leu Asn Glu Gln Ser Ser Tyr His Thr Gln Cys Asp Ile Asp
235 125                 130                 135                     140
238 Tyr Ser Ser Gln Ser Ser Ile Glu Thr Cys Trp Ile Ser Gly Leu Pro
239                 145                 150                 155
242 Asp Leu Asp Thr Thr Asp Ser Thr Ile Arg Ser Leu Phe Gln Thr Trp
243             160                 165                 170
246 Val His Gly Leu Val Ser Asn Tyr Ser Phe Asp Gly Leu Arg Val Asp
247         175                 180                 185
250 Thr Val Lys His Val Glu Lys Asp Tyr Trp Pro Gly Phe Val Ser Ala
251     190                 195                 200
254 Ala Gly Thr Tyr Ala Ile Gly Glu Val Phe Ser Gly Asp Thr Ser Tyr
255 205                 210                 215                     220
258 Val Ala Gly Tyr Gln Ser Val Met Pro Gly Leu Leu Asn Tyr Pro Ile
259                 225                 230                 235
262 Tyr Tyr Pro Leu Ile Arg Val Phe Ala Gln Gly Ala Ser Phe Thr Asp
263             240                 245                 250
266 Leu Val Asn Asn His Asp Thr Val Gly Ser Thr Phe Ser Asp Pro Thr
267         255                 260                 265
270 Leu Leu Gly Asn Phe Ile Asp Asn His Asp Asn Pro Arg Phe Leu Ser
271     270                 275                 280
274 Tyr Thr Ser Asp His Ala Leu Leu Lys Asn Ala Leu Ala Tyr Val Ile
275 285                 290                 295                     300
278 Leu Ala Arg Gly Ile Pro Ile Val Tyr Tyr Gly Thr Glu Gln Gly Tyr
279             305                 310                 315
282 Ser Gly Ser Ser Asp Pro Ala Asn Arg Glu Asp Leu Trp Arg Ser Gly
283             320                 325                 330
286 Tyr Ser Thr Thr Gly Asp Ile Tyr Thr Thr Ile Ala Ala Leu Ser Ala
287         335                 340                 345
290 Ala Arg Thr Ala Ala Gly Gly Leu Ala Gly Asn Asp His Val His Leu
```

```
291      350                  355                  360
294 Tyr Thr Thr Asp Asn Ala Tyr Ala Trp Ser Arg Ala Ser Gly Lys Leu
295 365              370              375              380
298 Ile Val Val Thr Ser Asn Arg Gly Ser Ser Asp Ser Ser Thr Ile Cys
299              385              390              395
302 Phe Ser Thr Gln Gln Ala Ser Gly Thr Thr Trp Thr Ser Thr Ile Thr
303              400              405              410
306 Gly Asn Ser Tyr Thr Ala Asp Ser Asn Gly Gln Ile Cys Val Gln Leu
307          415              420              425
310 Ser Ser Gly Gly Pro Glu Ala Leu Val Val Ser Thr Ala Thr Gly Thr
311      430              435              440
314 Ala Thr Ala Thr Thr Leu Ser Thr Thr Thr Lys Thr Ser Thr Ser Thr
315 445              450              455              460
318 Ala Ser Cys Ala Ala Thr Val Ala Val Thr Phe Asn Glu Leu Val Thr
319              465              470              475
322 Thr Asn Tyr Gly Asp Thr Ile Arg Leu Thr Gly Ser Ile Ser Gln Leu
323          480              485              490
326 Ser Ser Trp Ser Ala Thr Ser Gly Leu Ala Leu Ser Ala Ser Ala Tyr
327          495              500              505
330 Thr Ser Ser Asn Pro Leu Trp Ser Val Thr Val Ser Leu Pro Ala Gly
331      510              515              520
334 Thr Ser Phe Glu Tyr Lys Phe Val Arg Ile Thr Ser Asp Gly Thr Val
335 525              530              535              540
338 Thr Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr Cys Ala
339              545              550              555
342 Ser Thr Ala Thr Ile Ser Asn Thr Trp Arg
343          560              565
346 <210> SEQ ID NO: 3
347 <211> LENGTH: 18
348 <212> TYPE: DNA
349 <213> ORGANISM: Artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: Primer amyD1
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (3)..(3)
358 <223> OTHER INFORMATION: n is a, c, g, or t
360 <220> FEATURE:
361 <221> NAME/KEY: misc_feature
362 <222> LOCATION: (12)..(12)
363 <223> OTHER INFORMATION: n is a, c, g, or t
365 <400> SEQUENCE: 3
366 gsntaccayg gntactgg                                          18
369 <210> SEQ ID NO: 4
370 <211> LENGTH: 17
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Primer amyD2R
```

W-->

RAW SEQUENCE LISTING ERROR SUMMARY    DATE: 07/21/2006
PATENT APPLICATION:  US/10/585,620    TIME: 17:42:24

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\07212006\J585620.raw**

**Please Note:**
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3;  N Pos.  3,12
Seq#:4;  N Pos.  15
Seq#:5;  N Pos.  15
Seq#:6;  N Pos.  3,6,15
Seq#:7;  N Pos.  3,6,15
Seq#:8;  N Pos.  3,6,15
Seq#:13; Xaa Pos. 9

**Invalid <213> Response:**
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,14,15,16,17

**VERIFICATION SUMMARY**                          DATE: 07/21/2006
PATENT APPLICATION:  **US/10/585,620**            TIME: 17:42:24

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\07212006\J585620.raw**

```
L:11  M:270 C: Current Application Number differs, Replaced Current Application No
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
```

# Raw Sequence Listing before editing
## (for reference only)

IFWP

**RAW SEQUENCE LISTING**          DATE: 07/19/2006
PATENT APPLICATION:  **US/10/585,620**          TIME: 08:29:59

Input Set : **A:\01-SQ Listing-06 Jul 2006.txt**
Output Set: **N:\CRF4\07192006\J585620.raw**

```
   3 <110> APPLICANT: Ye, Liu
   4         Lan, Tang
   5         Spendler, Tina
   7 <120> TITLE OF INVENTION: Amylase
   9 <130> FILE REFERENCE: 10583.204-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/585,620
C--> 11 <141> CURRENT FILING DATE: 2006-07-08
  11 <160> NUMBER OF SEQ ID NOS: 17
  13 <170> SOFTWARE: PatentIn version 3.3
```

*Does Not Comply
Corrected Diskette Needed*

**ERRORED SEQUENCES**

```
 594 <210> SEQ ID NO: 17
 595 <211> LENGTH: 29
 596 <212> TYPE: DNA
 597 <213> ORGANISM: Artificial
 599 <220> FEATURE:
 600 <223> OTHER INFORMATION: Primer AM835.2
 602 <400> SEQUENCE: 17
 603 cgtctcgagg acacaacgaa aaagcatca                                      29
E--> 609 11
```

**RAW SEQUENCE LISTING ERROR SUMMARY**     DATE: 07/19/2006
PATENT APPLICATION:  **US/10/585,620**     TIME: 08:30:00

Input Set : **A:\01-SQ Listing-06 Jul 2006.txt**
Output Set: **N:\CRF4\07192006\J585620.raw**

<u>Invalid <213> Response:</u>
**Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.**

Seq#:3,4,5,6,7,8,9,10,11,12,14,15,16,17

**VERIFICATION SUMMARY**               DATE: 07/19/2006
PATENT APPLICATION:  **US/10/585,620**      TIME: 08:30:00

Input Set : **A:\01-SQ Listing-06 Jul 2006.txt**
Output Set: **N:\CRF4\07192006\J585620.raw**

```
L:11  M:270 C: Current Application Number differs, Replaced Current Application No
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:609 M:254 E: No. of Bases conflict, this line has no nucleotides.
```